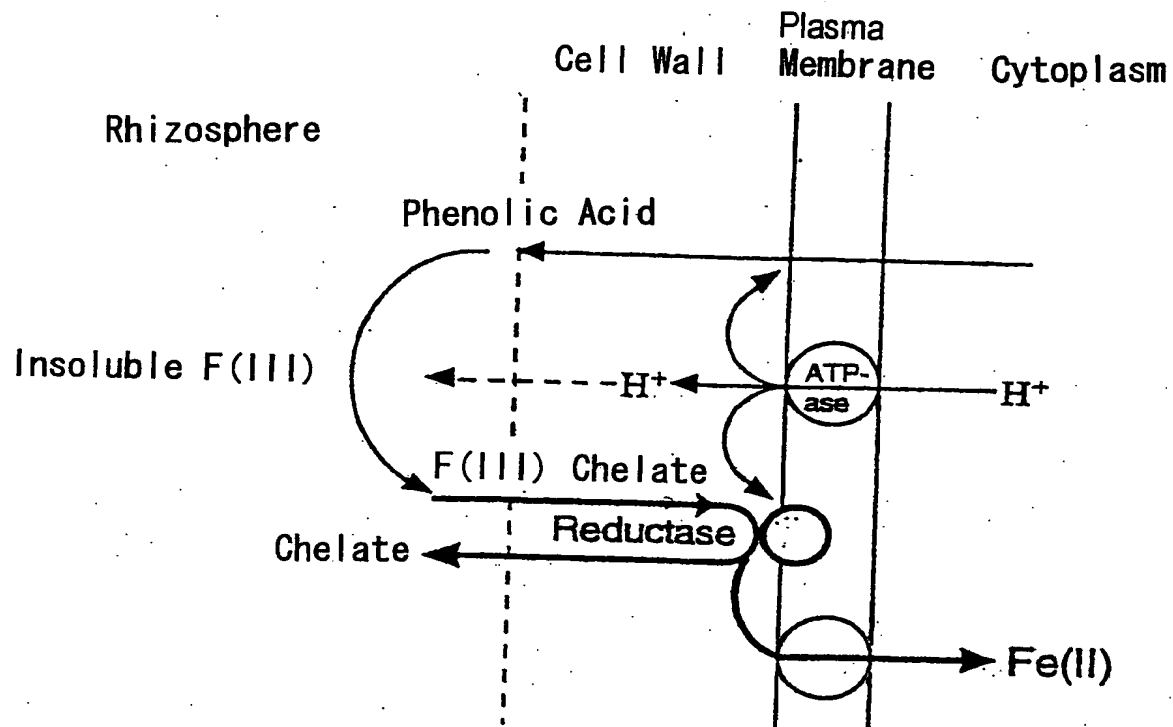
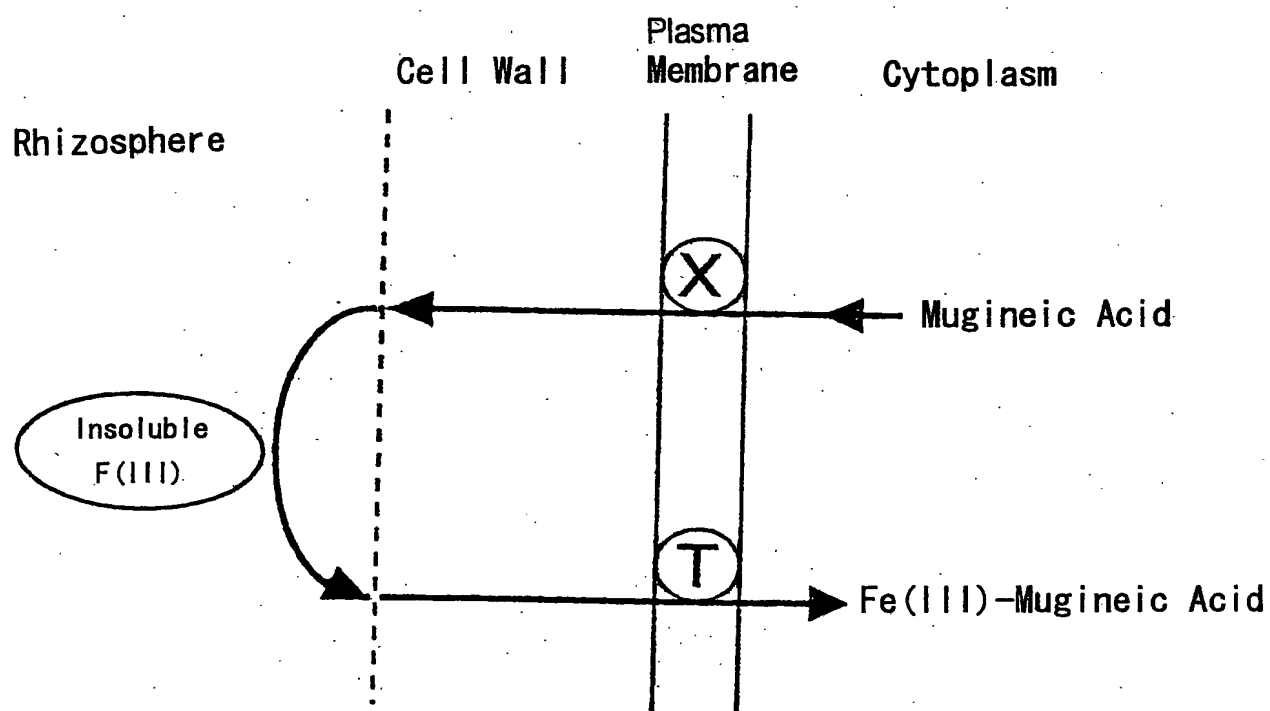


Fig. 1



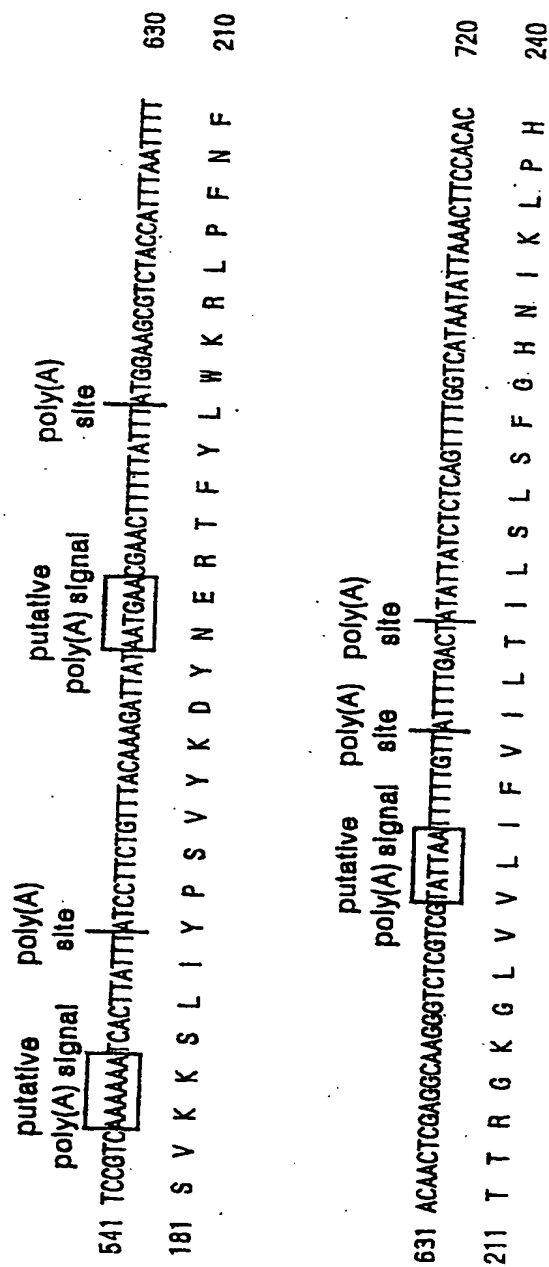
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Fig. 2



Two Kinds of Fe-Uptake Mechanisms in Higher Plants

Fig. 3



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Fig. 5

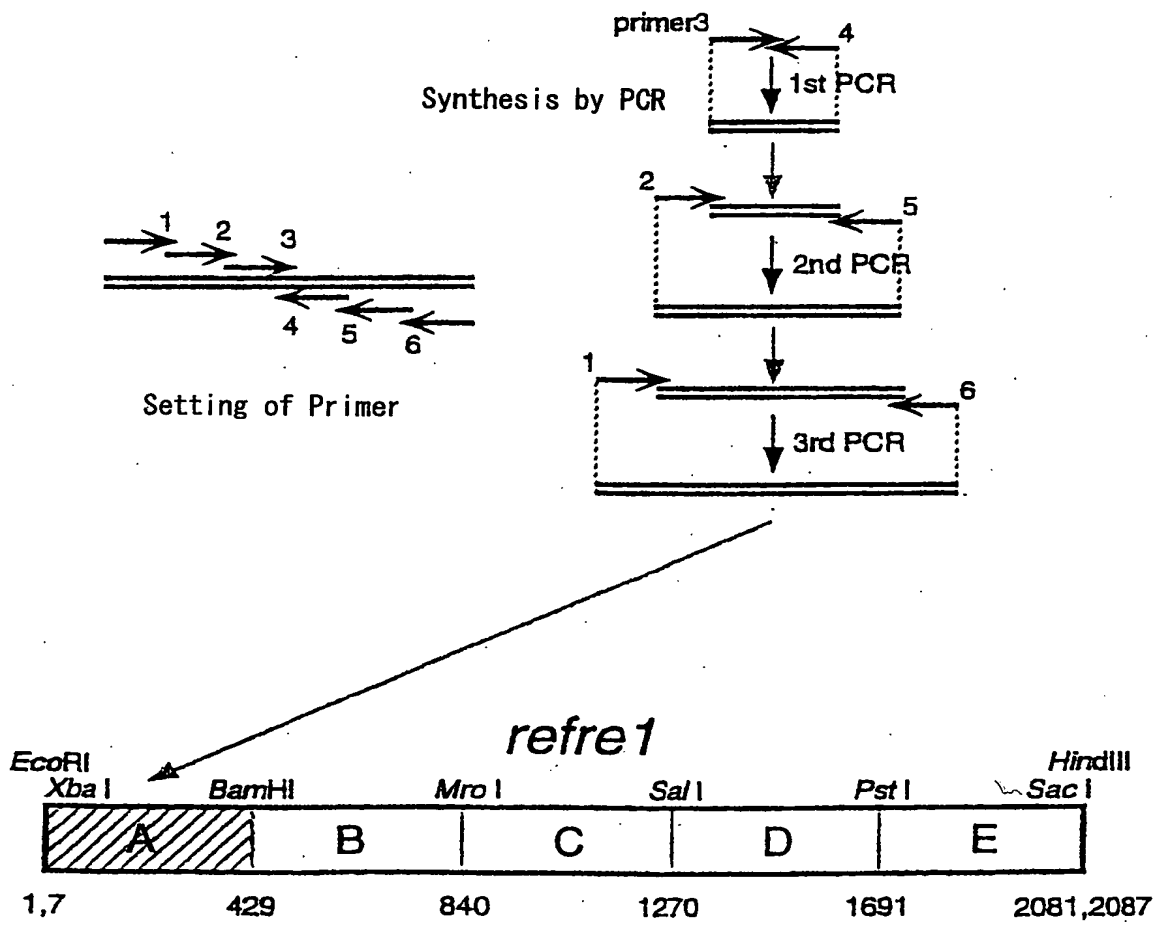


Fig. 6

Sequence Name Base Sequence

	5'		3'
A-1	GAATTCCTAGACTCCACCATGGTTAGAACCAGAGTCCTTTCTGCTCTTCATCTCTTCTTCGCTACAGTCCAAATGAGGG	83mer	
A-2	GTCCAAATGAGGGCTACACTCATCTCCACTTCATGCATTTCTCAGGCTGCACTGTACCAAGTTGCGATGCTCAAGCAAGTCAAA	83mer	
A-3	CAAGCAAGTCAAAGTCTTGCTACTGCAAGAACATCAATTGGCTCGGAAGGGTCACTGCGATGCGCTTATGAGAACTCCAAATCT	83mer	
A-4	TCCAGTGTGTAACCTTGACTCTGAGCATTGGCTGGCAAGTTTCATCAAAGGGAGTCCAGAGTCTTGTATAGATTGGAGTT	83mer	
A-5	TGCTCTCTATCGGATTTCTCAGGAGGGGAAGGTAGTTACTTGCATTAAAGGTAGATGTTCTTCATGTCTCCAGTGTGTAAA	83mer	
A-6	GGATCCCATAGTTTCTCATAGTAGTAGTGATAGGCGCTCTCATTGGCATCAAGGTTGTGAAACAACGTCTCTCTATCG	83mer	
B-1	GGATCCACTTGAATTTGATGCGATCTCAATGGTGGCATGGGGCTGGTCTTCTTCTGGGTGCGAGTCTTAACGGGSCA	80mer	
B-2	CCTTACGGGGCAACTATCTTGAACATTCTCAAAGCGGATTTGGCAAGAACATTATGGCAAAATCTGTAAAGAGTCTC	80mer	
B-3	GTTAAGAGTCTCTTATCTACCCAGCGTTTACAAGAGCTACAGAGAGAACTTCTATCTTTGGAAAGTTTGGCATT	80mer	
B-4	AGAGTGAGAGATAGTCAGAAATGACAAGATAAGAACTACAGTCTCTTGGCTGAGTTGTAAAGTTGAATGGCAAGGT	80mer	
B-5	AATGCCATTGATCTTCTCCATCTAGGTCTATCGTAAGGATGTGGCAACTTGATGTTATGTCCGAAAGAGAGTGAGAGAT	80mer	
B-6	TCCGGATACGAAAGGTACACCAAGGGGAAAGAGCGATTGGCATCAAGTCAGCAAGCGGTGAGAGCAATGCCATTGAT	80mer	
C-1	TCCGACAAACCCCTTCATCCCAATCAAGGATTGAGCTTTAGTACTTTCAACTTTTACACAAATGGTCAGCATAGTCTGC	83mer	
C-2	GCATAGTCTGCTTCATGTTAGCGGTGCTCCATTCATCGTTATGACCGCTTCAGGAGTTAAAGAGGAGTATTCAGTCTCT	83mer	
C-3	TATTCCAGTCTCTTGTAAAGAAATCTTACTTCAGATGGGGAATAGTAGCCAACTTCTTATGTCCATCATCTTTCCAGTGC	83mer	
C-4	ATAACATGATGTTTATGCTTTTGTGAATAAGTAAGAGATTTCATAACCTGGTTCCTGAAGACCTTCGAGCTGMAAAT	83mer	
C-5	GAGGATGCCAGCCATGCAACAGATCCAGCCATCCATCTAGTGTGTGGCAATGTAATACATAGCTATGATAAACATGATGT	83mer	
C-6	GTCGACAAAGTGGGGTCTTAAGACCTCGTTCATGATGATAGTACAATTGGCAGAACCTGTGAGGAGAGGATGCCAGC	83mer	
D-1	GTGACCAAGATGATCTTAAGTTATCAAGATCTCTGTCAAGAGCCTAAGTCTTCAAGTATCAAGTGGAGCATTTGCC	82mer	
D-2	GGAGCATTTGCTATATGTAATCTTTTCAACAAATCAGCGTGGTCTACAGTTTTCATCTCATCTCTTACAGTCTAT	82mer	
D-3	TTACAGTCTTATCAGAAAGGCACAGATCTTAAACACCAAGATCACTAATATGTAAGTCAAAGCTAACAAAGGCATTAA	82mer	
D-4	CCTCTAAGAAATCTTGAATCAAGGTATGGTTTGGAGCGCTTAGAAGTTTGGTAAGAGTACTCTGTAATGCGCTTGT	82mer	
D-5	GGCGGAGCTACTCTACTAGATTTCTCTTAAGTTTGGCAATGTGAGGGACAGTTACGCCATATGTTCTCTAAGAAAT	82mer	
D-6	CTGAGTTGATCAGTCTAGGCAATCTAAGGATCTTACGAAATGGGGTAGATGGCTGCCAGCGGAGGCGGAGCTACT	82mer	
E-1	CTGAGCACAAGTTCTACTGGATGTCACGACCTTAGTCAOCTTAAGTGGTTGAAAACGAGCTACATGGCTTAA	77mer	
E-2	ACATGGCTTAAAGAGAAATCTTGTGAGTCTCTGTCTACTAGGTCATCAGTGGAGGATACAACTCAGATG	77mer	
E-3	CAAACTCAGATGAGTCCACTAAGGGTTTGGATGACAAAGGAATCTGAAATCAAGTAGAATGCTTAAACAGAGG	77mer	
E-4	GTGATGTTGTGTTCTGAGTCTGACAAATGATCTCTGATCTCACTAGCTCTTTGAGTCTGGGCTCTGTGTAAG	77mer	
E-5	CGATACCTTGTACACTGCATTTCTAAAGTGGTCAATGAAAGTGGTGGCATGAGTAGAAAGTATGTTGTG	77mer	
E-6	AAGCTTGAGCTCTTACCAAGTAAACTCTCTCTCTAGTTTGCATCTATCTTCAGACTAGAATGATACCTTGTA	77mer	

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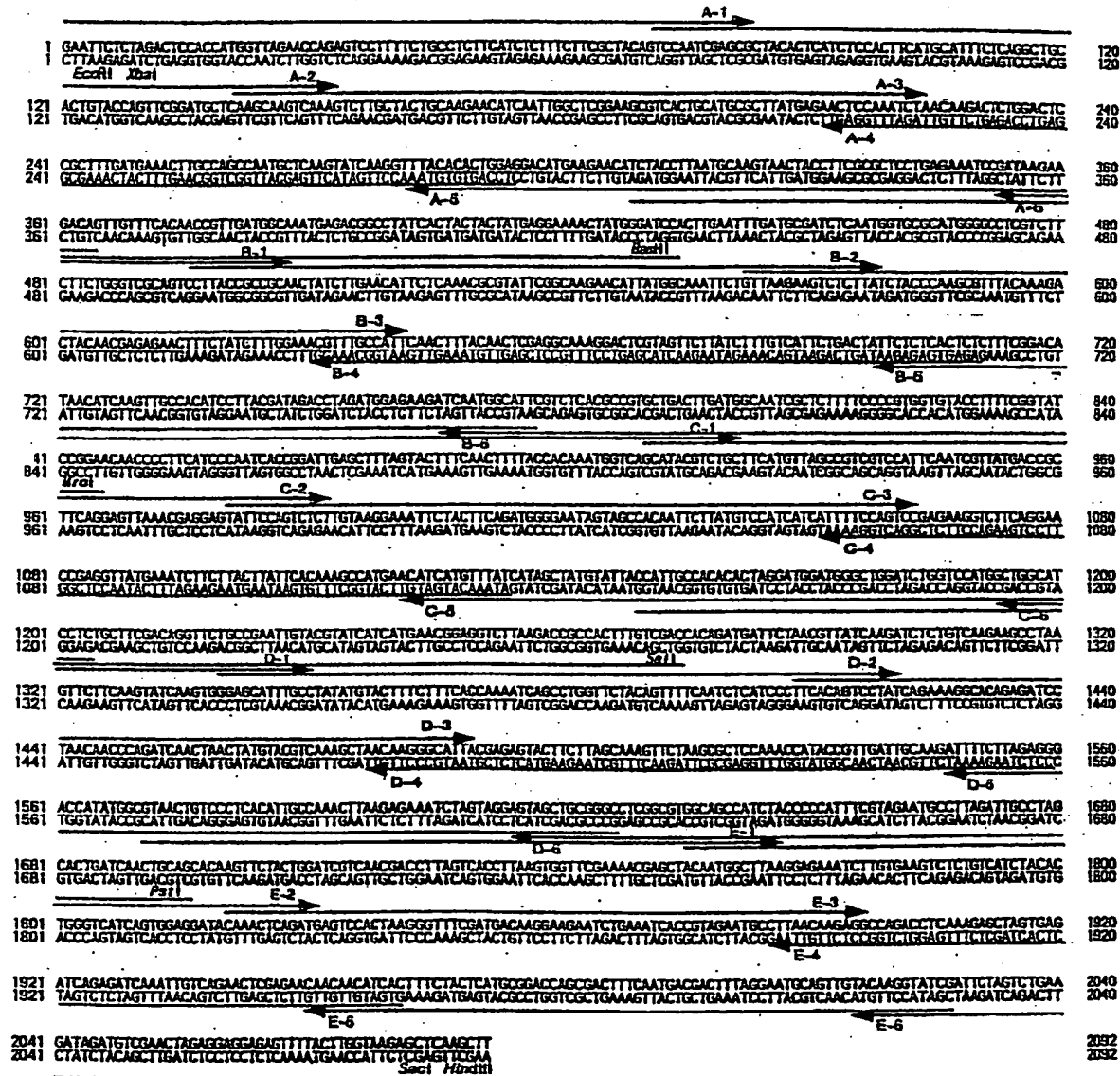


Fig. 8

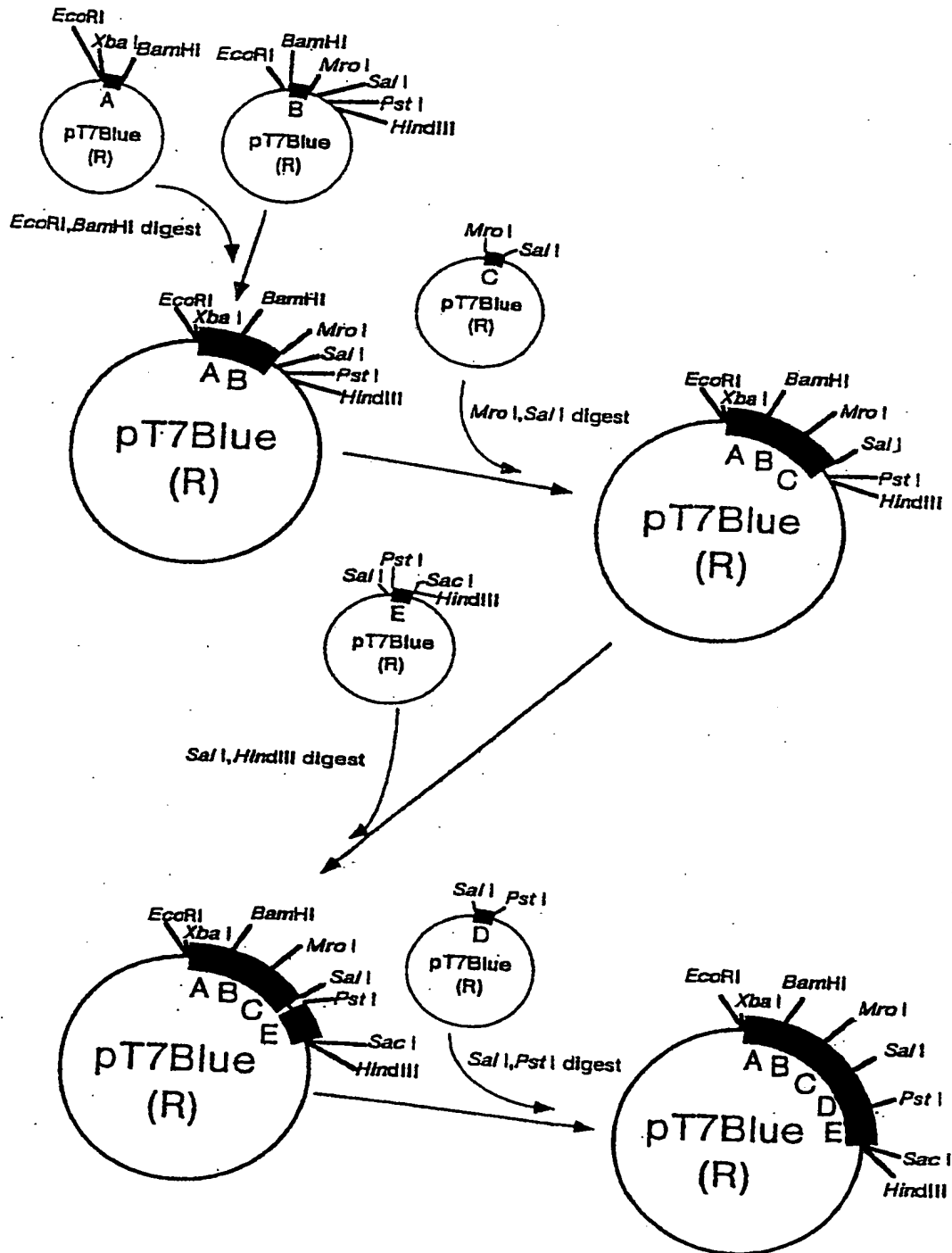


Fig. 9

1	gaattctctagactccacc	19
20	ATGGTTAGAACCASAGTCTTTTCTGCTCTCTCATCTCTTCTTCTGCTACAGTCCAATCGAGCGCTACACTCATCTCCACTTCATGCAATT	109
1	I M V R T R V L F C L F I S F F A T V Q S S A T L I S T S C I	30
110	TCTCAGGCTGCACGTACCACTGCGATGCTCAAGCAAGTCAAAGTCTGCTACTGCAAGAACATCAATTGCTCGGAAGCGTCACTGCA	199
31	S Q A A L Y O F G C S S K S X S C Y C K N I N W L G S V T A	60
200	TGCGCTTATGAGAACTCCAAATCTAACAAGACTCTGCACTCCGCTTTGATGAACTTGCCAGCCATGCTCAAGTATCAAGGTTTACACA	289
61	C A Y E N S K S N K T L D S A L M K L A S Q C S S I K Y Y T	90
290	CTGGAGGACATGAAGAACATCTACCTTAATGCAAGTAACCTCTCGGCTCTGAGAAATCGATAGAAGACAGTGTGTTTCAACAACCG	379
91	L E D M K N I Y L N A S N Y L R A P E K S D K K T V V S Q P	120
380	TTGATGGCAATGAGACGGGCTATCACTACTACTATGAGGAAACTATGGGATCCACTTGAATTTGATGCGATCTCAATGGTGGCATGG	469
121	L M A N E T A Y H Y Y Y E E N Y G I H L N L M R S O W C A W	150
470	GGGCTGCTTCTTCTGCGGCTGCGAGTCTTACCGCGCACTATCTTGAACATCTCAAGCGGTATTCGGCAAGAACATTATGGCAAT	559
151	G L V F F W V A V L T A A T I L N I L K R V F G K N I M A N	180
560	TCGTGTAAGAGTCTTATCTACCAAGCGTTTACAAGACTACACGAGAGAACTTCTATCTTTGGAACGTTTGCCATTCACTTT	649
181	S V K K S L I Y P S V Y K D Y H E R T F Y L W K R L P F N F	210
650	ACAACTCGAGGCAAGGACTCGTAGTCTTATCTTTGTCATTCTGACTATTCTCTCACTCTCTTTGGGACATAACATCAAGTTGCCACAT	739
211	T T R G K G L V L I F V I L T I L S L S F G H N I K L P H	240
740	CGTTACGATAGACTAGATGAGAGATCAATGGCATTGCTTCACGCGGCTGCTGACTTGATGGCAATCGCTCTTTTCCCGGTGGTGAC	829
241	P Y D R P R W R R S M A F V S R R A D L M A I A L F P V V Y	270
830	CTTTTGGTATCGGAAACACCGCTTATCCCAATCACCGGATTGAGCTTTAGTACTTTCACTTTTACCACAAATGGTCAGCATACGTC	919
271	L F G I R N N P F I P I T G L S F S T F N F Y H K W S A Y V	300
920	TGCTTCATGTTAGCGGCTGCTCCATTCAATCGTTATGAGCGCTTCAGGAGTTAAACGAGGAGTATTCAGTCTCTTGTGAAGGAATTCAC	1009
301	C F M L A V V H S I V M T A S S V K R G V F Q S L V R K F Y	330
1010	TTAGATGGGGAATAGTAGCCCAATCTTATGTCATCATCATTTTCCAGTCCGAGAAGGCTTTCAGGAACGAGGTTATGAAATCTTC	1099
331	F R W G I V A T I L M S I I I F Q S E K V F R N R G Y E I F	360
1100	TTACTTATTCACAAAGCCATGAACATCATGTTTATCATAGCTATGATTACCATTCGCACACTAGGATGGATGGGCTGGATCTGGTCC	1189
361	L L I H K A M N I M F I I A M Y Y H C H T L G W H G W I N S	390
1190	ATGGCTGGCATCTCTGCTTCGACAGGTTCTGCGGAATTGTACGTATCATGCAACGAGGCTTAAAGACCGGCACTTTGTGACCAACA	1279
391	M A G I L C F D R F C R I V R I L M N G G L K T A T L S T T	420
1280	GATGATTCTAAGCTTATCAAGATCTCTGTCAAGAGCGCTAAGTCTTCAAGTATCAAGTGGGAGCATTTCGCTATATGTACTTTCTTTCA	1369
421	D D S R V I K I S V K K P K F K Y Q V G A F A Y M Y F L S	450
1370	CCAAATCAGCGTGGTCTCAGATTTTCAATCTCATCGCTTACAGTCTTATCAGAAAGCACAGAGATCTTAACAACCCAGATCACTA	1459
451	P K S A W F Y S F Q S H P F T V L S E R H R D P N N P D Q L	480
1460	ACTATGTACGCTAAGCTAACAAGGCAATTACGAGAGTACTTCTTAGCAAGTTCTAAGCGCTCCAAACCATACCGTTGATTGCAAGATT	1549
481	T M Y Y K A N K G I T R V L L S K V L S A P N H T V D C K I	510
1550	TTCTTAGAGGACCATATGCGGTAACCTGCTCATTGCCAACTTAAGAGAAATCTAGTAGGAGTAGCTGCGGCTCGGCGTGGCA	1639
511	F L E G P Y G V T V P H I A K L K R N L V G V A A G L G V A	540
1640	GCCATCTACCCCATTTGCTAGAAATGCTTAGATTGCTAGCACTGATCAACTGCAGCACAAGTCTTACTGGATGCTCAAGGACTTAGT	1729
541	A I Y P H F V E C L R L P S T D Q L Q H K F Y W I V N D L S	570
1730	CACCTTAAGTGGTTCGAAAACGAGCTACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACACTGGGTCATCAGTGGAGAT	1819
571	H L K W F E N E L Q W L K E K S C E V S V I Y T G S S V E D	600
1820	ACAACCTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGATCTGAAATCACCGTAGAATGCTTAACAAGAGGCCAGCTCAAA	1909
601	T N S D E S T K G F D D K E E S E I T V E C L N K R P D L K	630
1910	GAGCTAGTGAGATCAGAGATCAATTTGTGAGAACTGAGAACCAACATCACTTTCTACTCATGCGGACCGAGCTTTCAATGACGAC	1999
631	E L V R S E I K L S E L E N N N I T F Y S C G P A T F N D D	660
2000	TTTAGGAATGAGTGTACAAGTATGATTCTAGTCTGAGATAGATGTCGAACCTAGAGGAGGAGATTTTACTTGGTAAgagctcaag	2089
661	F R N A V V Q G I D S S L K I D V E L E E E S F T W	687
2090	ctt	2092

Fig. 10

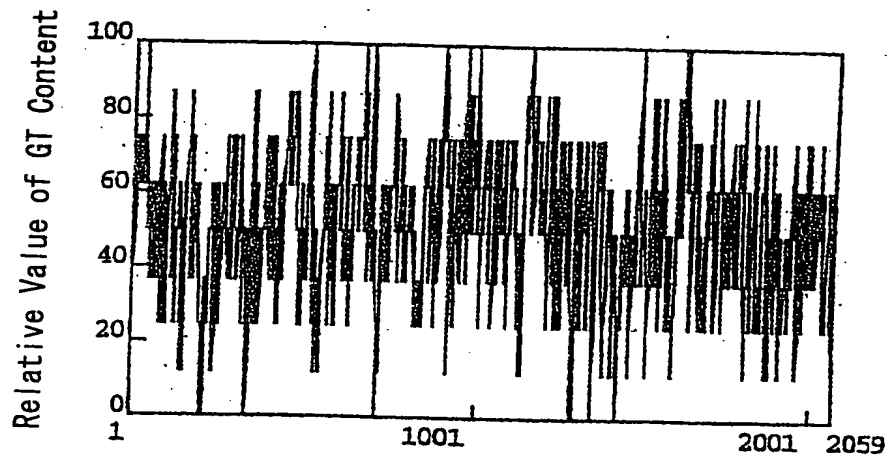
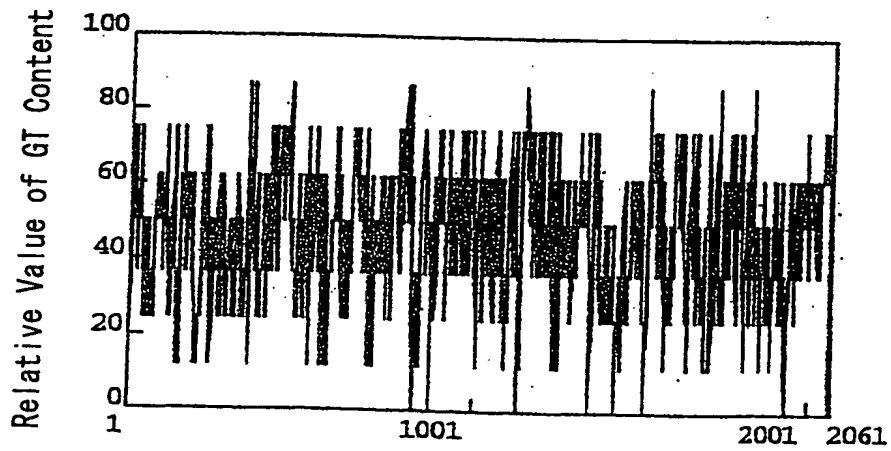
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Fig. 11

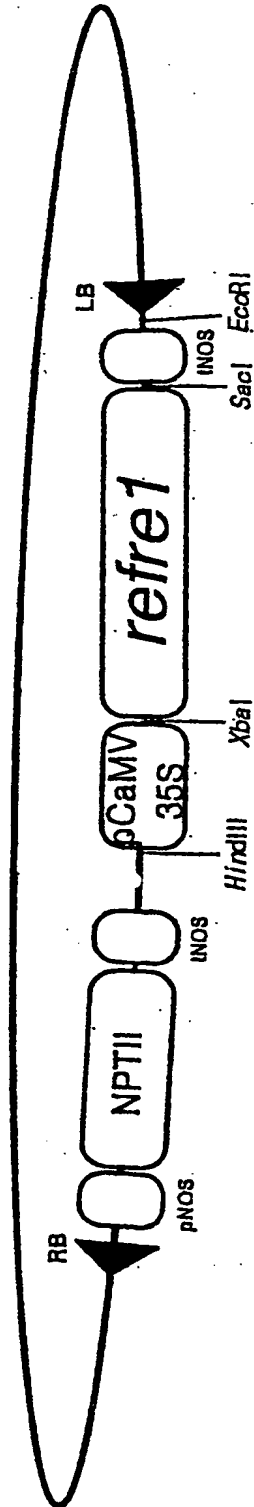


Fig. 12



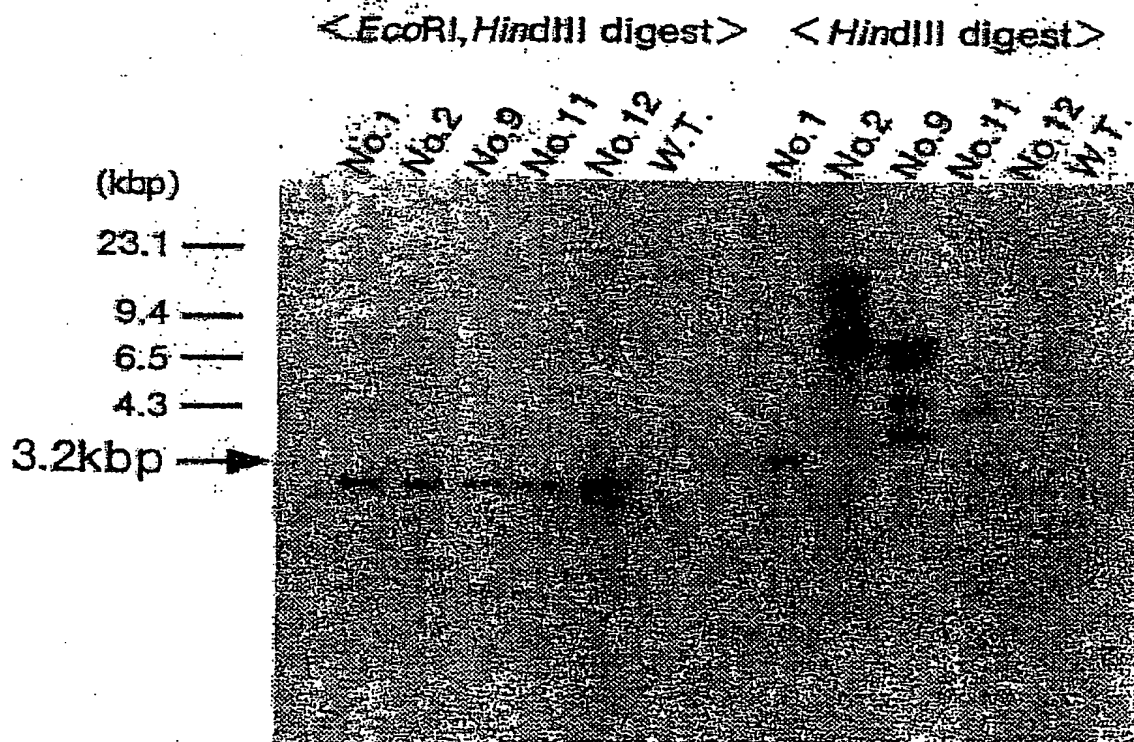
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Fig. 13



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Fig. 14



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Fig. 15

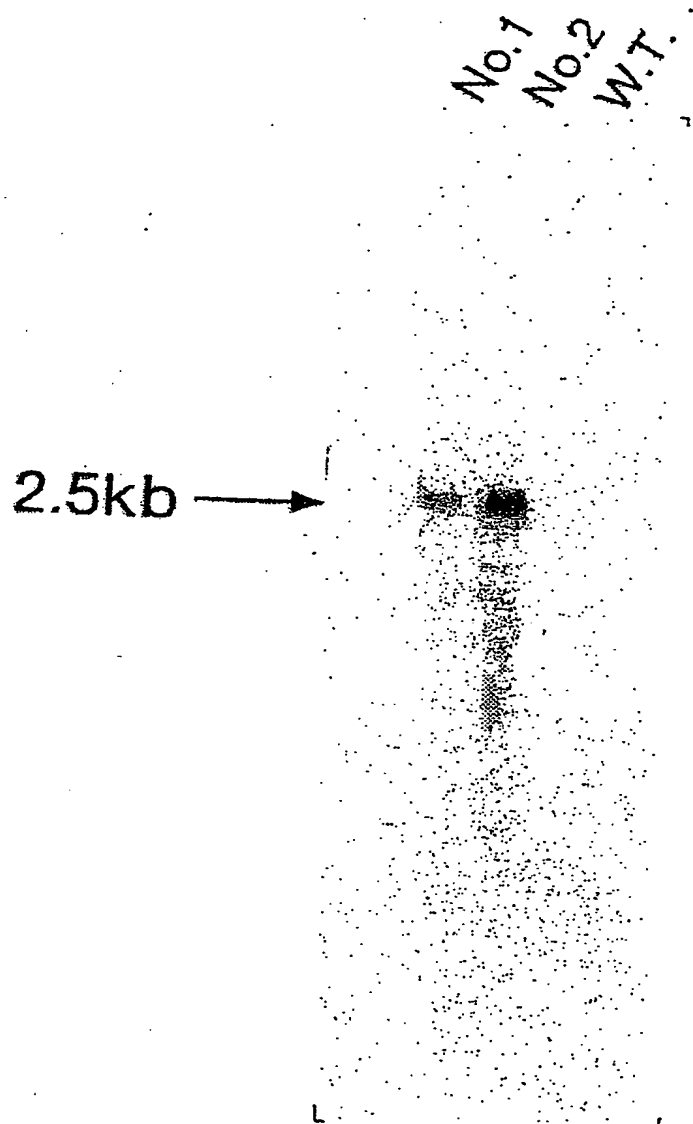


Fig. 16



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Fig. 17



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Fig. 18

 T_2 Plants